

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hawkins, Phillip R.
Murry, Lynn E.
- (ii) TITLE OF THE INVENTION: HUMAN PHOSPHOLIPASE INHIBITOR
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: U.S.
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Luther, Barbara J.
(B) REGISTRATION NUMBER: 33,954
(C) REFERENCE/DOCKET NUMBER: PF-0059-1 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1LPB02
(B) CLONE: CONSENSUS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

NCAATGGGCC GGCCGTGGGA AGGGTGAATG TGGGTCCAGA CCCGCCCTC CTCAGCTTCC

60

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TATAAAAGCT GGGGACCAGG TACTGCTGAT ACACACACCA TGAGGCTCTC CAGGAGACCA 120
GAGACCTTTC TGCTGGCCTT TGTGTTGCTC TGCACCCTCC TGGGTCTTGG GTGCCCCACTA 180
CACTGCGAAA TATGTACGGC GCGGGGAGC AGGTGCCATG GCCAAATGAA GACCTGCAGC 240
AGTGACAAGG ACACATGTGT GCTCCTGGTC GGGGAAGGCTA CTTCAAAGGG CAAGGAGTTG 300
GTGCACACCT ACAAGGGCTG CATCAGGTCC CAGGACTGCT ACTCCGGCGT TATATCCACC 360
ACCATGGGCC CCAAGGACCA CATGGTAACC AGCTCCTTCT GCTGCCAGAG CGACGGCTGC 420
AACAGTGCCT TTTTGTCTGT TCCCTTGACC AATCTTACTG AGAATGGCCT GATGTGCCCC 480
GCCTGCACTG CGAGCTTCAG GGACAAATGC ATGGGGCCCA TGACCCACTG TACTGGAAAG 540
GAAAACCACT GCGTCTCCTT ATCTGGACAC GTGCAGGCTG GTATTTTCAA ACCCAGATTT 600
GCTATGCGGG GCTGTGCTAC AGAGAGTATG TGCTTTACCA AGCCTGGTGC TGAAGTACCC 660
ACAGGCACCA ATGTCTCTT CCTCCATCAT ATAGAGTGCA CTCACTCCCC CTGAAAAGCT 720
ATCTGAACAG AGGAAGATAA TGTAGTGTGA AGTCCCCATT TGTCTCAGC CTGTAACCTC 780
CCCGTGTGCC TATAAGAAG TTAATAGAGC AAAAAAAAAA AAAAAAAAAA AAACCTCGAG 839

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: CONSENSUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Arg Leu Ser Arg Arg Pro Glu Thr Phe Leu Leu Ala Phe Val Leu
 1           5           10           15
Leu Cys Thr Leu Leu Gly Leu Gly Cys Pro Leu His Cys Glu Ile Cys
 20           25           30
Thr Ala Ala Gly Ser Arg Cys His Gly Gln Met Lys Thr Cys Ser Ser
 35           40           45
Asp Lys Asp Thr Cys Val Leu Leu Val Gly Lys Ala Thr Ser Lys Gly
 50           55           60
Lys Glu Leu Val His Thr Tyr Lys Gly Cys Ile Arg Ser Gln Asp Cys
 65           70           75           80
Tyr Ser Gly Val Ile Ser Thr Thr Met Gly Pro Lys Asp His Met Val
 85           90           95
Thr Ser Ser Phe Cys Cys Gln Ser Asp Gly Cys Asn Ser Ala Phe Leu
100           105           110
Ser Val Pro Leu Thr Asn Leu Thr Glu Asn Gly Leu Met Cys Pro Ala
115           120           125
Cys Thr Ala Ser Phe Arg Asp Lys Cys Met Gly Pro Met Thr His Cys
130           135           140
Thr Gly Lys Glu Asn His Cys Val Ser Leu Ser Gly His Val Gln Ala
145           150           155           160
Gly Ile Phe Lys Pro Arg Phe Ala Met Arg Gly Cys Ala Thr Glu Ser
165           170           175
Met Cys Phe Thr Lys Pro Gly Ala Glu Val Pro Thr Gly Thr Asn Val
180           185           190
Leu Phe Leu His His Ile Glu Cys Thr His Ser Pro
195           200

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI 501050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Lys	Tyr	Leu	His	Thr	Ile	Cys	Leu	Leu	Phe	Ile	Phe	Val	Ala	Arg	1	5	10	15
Gly	Asn	Ser	Arg	Ser	Cys	Asp	Phe	Cys	His	Asn	Ile	Gly	Lys	Asp	Cys	20	25	30	
Asp	Gly	Tyr	Glu	Glu	Glu	Cys	Ser	Ser	Pro	Glu	Asp	Val	Cys	Gly	Lys	35	40	45	
Val	Leu	Leu	Glu	Ile	Ser	Ser	Ala	Ser	Leu	Ser	Val	Arg	Thr	Val	His	50	55	60	
Lys	Asn	Cys	Phe	Ser	Ser	Ser	Ile	Cys	Lys	Leu	Gly	Gln	Phe	Asp	Val	65	70	75	80
Asn	Ile	Gly	His	His	Ser	Tyr	Ile	Arg	Gly	Arg	Ile	Asn	Cys	Cys	Glu	85	90	95	
Lys	Glu	Leu	Cys	Glu	Asp	Gln	Pro	Phe	Pro	Gly	Leu	Pro	Leu	Ser	Lys	100	105	110	
Pro	Asn	Gly	Tyr	Tyr	Cys	Pro	Gly	Ala	Ile	Gly	Leu	Phe	Thr	Lys	Asp	115	120	125	
Ser	Thr	Glu	Tyr	Glu	Ala	Ile	Cys	Lys	Gly	Thr	Glu	Thr	Lys	Cys	Ile	130	135	140	
Asn	Ile	Val	Gly	His	Arg	Tyr	Glu	Gln	Phe	Pro	Gly	Asp	Ile	Ser	Tyr	145	150	155	160
Asn	Leu	Lys	Gly	Cys	Val	Ser	Ser	Cys	Pro	Leu	Leu	Ser	Leu	Ser	Asn	165	170	175	
Ala	Thr	Phe	Glu	Gln	Asn	Arg	Asn	Tyr	Leu	Glu	Lys	Val	Glu	Cys	Lys	180	185	190	
Asp	Ala	Ile	Arg	Leu	Ala	Ser	Leu									195	200		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

PF-0059-5 CON

- (A) LIBRARY: HMC1N0T01
- (B) CLONE: 8941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAGGCCTAG	GGTTAGGCAA	GACCTTGAGG	CAGGGGTTGA	AGCCAGGGAG	TGGTCAGCCA	60
GCACTGTCCC	TGCCTGTCCC	CATCCCACAG	AGGGCAAGGA	GTTGGTGCAC	ACCTACAAGG	120
GCTGCATCAG	GTCCCAGGAC	TGCTACTCCG	GCGTTATATC	NACCACCATG	GGCCCCAAGG	180
ACCACATGGT	AACCAGCTCC	TTCTGNTGCC	AGAGCGACGG	CTGCAACAGT	GCCTTTTTGT	240
CTGTTCCCTT	GACCAATCTT	ACTGAGAATG	GCCTGATGTG	CCCNGCTGCA	CTGCGAGTTT	300
NAGGGNCAAA	ATNCATGGGG	GCCCATT				327

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB01
- (B) CLONE: 10033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGCTCTNC	ACCCTCCTGG	GTCTTGGGTG	CCCACTACAC	TGCGAAATAT	GTACGGCGGC	60
GGGGAGCAGG	TGCCATGGCC	AAATGAAGAC	CTGCAGCAGT	GACAAGGACA	CATGTGTGCT	120
CCTGGTCGGG	AAGGCTACTT	CAAAGGGCAA	GGAGTTGGTG	CACACCTACA	AGGGCTGCAT	180
CAGGTCCAG	GACTGCTACT	CCGCGTTAT	ATCCACCACC	ATGGGCCCCA	AGGACCACAT	240
GGTAACCAGC	TCCTTCTGCT	GCAGAGCGAC	GGCTGCAACA	GTGCC'TTTT	GTCTGTTCCC	300
TTGACCAATC	TTACTGAGAA	TGGT				324

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB01
- (B) CLONE: 10644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACACATGTG	TNCTCCTGGT	CGGGAAGGCT	ACTTCAAAGG	GCAAGGAGTT	GGTGACACAC	60
TACAAGGGCT	GCATCAGGTN	CCAGGACTGC	TACTCCGGNG	TTATATCCAC	CACCATGGGC	120
CCCAAGGACC	ACATGGTAAC	CAGCTCCTTC	TGCTGCCAGA	GCGACGGCTG	CAACAGTGCC	180

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TTTTTGTCTG TTCCCTTGAC CAATNTTACT GAGAATNGNC TGATGTGCCC CGNCTGCACT	240
GNGAGCTTCA GGGACAAATG CT	262

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB01
- (B) CLONE: 10774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACACATGTG TGCTCCTGGT CGGGAAGGCT ACTTCAAAGG GCAAGGAGTT GGTGCACACC	60
TACAAGGGCT GCATCAGGTC CCAGGACTGC TACTCCGGNG TTATATCCAC CACCATGGGC	120
CCCAAGGACC ACATGGTAAC CAGCTCCTTC TGCTGCCAGA GCGACGGCTG CAACAGTGCC	180
TTTTTGTCTG TTCCCTTANC CAATCTTACT GAGAATGGCC TGATGTGCCC CGNCTGAACT	240
NCGAGCTTCA GGGACAAATN CATGGGNCNA TGACCCACTG TACTGGNAAG NNAAACCACT	300
GNGTGTCTT	310

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PEB01
- (B) CLONE: 71854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCCGGCGTT ATATCCACCA CCATGGGCCC CAAGGACCAC ATGGTAACCA GCTCCTTCTG	60
CTGCCAGAGC GACGGCTGCA ACANTGCCTT TTTNTNTGTT CCCTTGACCA ATCTTACTGA	120
GAATGGCCTG ATGTGCCCCG CCTGCACTGC GAGCTTCAGG GACAAATGCA TGGGGCCCAT	180
GACCC	185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1PEB01

(B) CLONE: 72861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGTGCAC	ACCTACAAGG	GCTGCATCAG	GTCCCAGGAC	TTCTACTCCG	GNGTTATATC	60
CACCACCATG	GGCCCCAAGG	ACCACATGGT	AACCAGCTCC	TTNTGCTGCC	AGAGCGACGG	120
CTGCAACATT	GCCTTTTTNT	NTGTNCCCTT	G			151

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1PEB01

(B) CLONE: 74452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGACTGCT	ACTCCGGNGT	TATATCCACC	ACCATGGGCC	CCAAGGACCA	CATGGTAACC	60
AGCTCCTTCT	GCTGCCAGAG	CNACGGCTGC	AACANTGCCT	TTNTGTCTGT	NCCCTTGACC	120
AATCTNACTG	AGAATNGCCT	GATT				144

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1LPB02

(B) CLONE: 155045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CNTGGCCTTA	GTTTTNCNCT	CACCCCTCCNG	GGTCTNGGGT	GCCCACNACA	CTGCGAANTA	60
TGTACGGCGG	CGGGTAGCAG	GTTCCATGNC	CAAATNAAGA	NCTTCANCNG	TGACAAGGAC	120
ACATGTNTGC	TCCTGGTCGG	NAAGNCTACT	TCAAAGGGCA	AGGAGTTGGT	GCAC	174

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: 156817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGCCTTTG	TGTTGCTCTG	CACCCTCCTG	GGTCTTGGGT	GCCCACTACA	CTGCGAAATA	60
TGTACGGCGG	CGGGGAGCAG	GTGCCATGGC	CAAATGAAGA	CCTGCAGCAG	TGACAAGGAC	120
ACATGTGTGC	TCCTGGTCGG	GAAGGCTACT	TCAAAGGGCA	AGGAGTTNGT	GCACACCTAC	180
AAGGGCTGCA	TCAT					194

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PGANNOT01
- (B) CLONE: 619856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAAGAGAC	CATNCCAGGA	AGTTGTGGGG	TTGGGGAGGC	CTAGGGTTAG	GCAAGACCTT	60
GAGGCAGGGG	TTGAAGCCAG	GGAGTGGTCA	GCCAGCACTG	TCCCTGCCTG	TCCCCATCCC	120
ACAGAGGGCA	AGGAGTTGGT	GCACAACTAC	AAGGGCTGCA	TCAGGTCCCA	GGACTGCTAC	180
TNCGGNGTTA	TATCCACCAC	CATGGGCCCC	AAGGACCACA	TGGT		224

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSN0T02

PF-0059-5 CON

(B) CLONE: 683480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTGGTGCAC	ACCTACAAGG	GCTGCATCAG	GTCCCAGGAC	TGCTACTCCG	GCGTTATATN	60
CACCACCATG	GGNCCCAAGG	ACCACATGGT	AACCAGCTCC	TTNTGCTGCC	AGAGCGACGN	120
CTGCAACAGT	GCCTTTTTGT	CTGTTCCCTT	GACCAATCTT	ACTGAGAATG	GCCTGATGTG	180
CCCCGNCTGC	ACTGCGAGCT	TNAGGGACAA	ATGCATGGGG	CCCATGACCC	ACTGTACTGG	240
AGAGGAAAAC	CA					252

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT11
- (B) CLONE: 1291208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

GGGAATCCCA	GTTCTTGCAG	CCACTGGGAA	TCAAGAGGCC	CAACTCCGTC	TTGGTCTTNN	60
NNNNNNNNNN	NNNNNNNNCA	TGGGCCGGCC	GTGGGAAGGG	TGAATGTGGG	TCCAGACCCG	120
CCCCTCCTCA	GCTTCCTATA	AAAGCTGGGG	ACCAGGTACT	GCTGATACAC	ACACCATGAG	180
GCTCTCCAGG	AGACCAGAGA	CCTTTCTGCT	GGCCTTTGTG	TTGCTCTGCA	CCCTCCTGGG	240
TCTTGGGTGC						250